



(19)

Europäisches Patentamt
European Patent Office
Office européen des brevets



(11)

EP 1 308 459 A2

(12)

EUROPEAN PATENT APPLICATION

(43) Date of publication:
07.05.2003 Bulletin 2003/19

(51) Int Cl.7: C07K 14/705, C12N 15/12,
C12N 5/10, C07K 16/18,
C12Q 1/68, G01N 33/68

(21) Application number: 02007401.9

(22) Date of filing: 28.03.2002

(84) Designated Contracting States:
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU
MC NL PT SE TR
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: 05.11.2001 JP 2001379298
25.01.2002 US 350978

(71) Applicants:
• Helix Research Institute
Kisarazu-shi, Chiba 292-0812 (JP)
• Research Association for Biotechnology
Tokyo 105-0003 (JP)

(72) Inventors:
• Isogai, Takao
Inashiki-gun, Ibaraki 300-0303 (JP)
• Sugiyama, Tomoyasu
Tokyo 130-0003 (JP)
• Otsuki, Tetsuji
Kisarazu-shi, Chiba 292-0055 (JP)
• Wakamatsu, Ai
Kisarazu-shi, Chiba 292-0014 (JP)
• Sato, Hiroyuki
Toyonaka-shi, Osaka 560-0021 (JP)
• Ishii, Shizuko
Kisarazu-shi, Chiba 292-0812 (JP)
• Yamamoto, Jun-ichi
Kisarazu-shi, Chiba 292-0041 (JP)

- Isono, Yuuko
Kisarazu-shi, Chiba 292-0014 (JP)
- Hio, Yuri
Kisarazu-shi, Chiba 292-0812 (JP)
- Otsuka, Kaoru
Honjo-shi, Saitama 367-0047 (JP)
- Nagai, Keiichi
Yamato-shi, Tokyo 207-0022 (JP)
- Irie, Ryotaro
Kisarazu-shi, Chiba 292-0801 (JP)
- Tamechika, Ichiro
Hirakata-shi, Osaka 573-0034 (JP)
- Seki, Naohiko
Chiba-shi, Chiba 261-0001 (JP)
- Yoshikawa, Tsutomu
Kisarazu-shi, Chiba 292-0043 (JP)
- Otsuka, Motoyuki
Tokyo 125-0062 (JP)
- Nagahari, Kenji
Tokyo 167-0053 (JP)
- Masuho, Yasuhiko
Koganei-shi, Tokyo 184-0011 (JP)

(74) Representative: VOSSIUS & PARTNER
Siebertstrasse 4
81675 München (DE)

Remarks:

The complete document including Reference Tables and the Sequence Listing is available on CD-ROM from the European Patent Office, Vienna sub-office

(54) Full-length cDNA sequences

(57) Novel full-length cDNAs are provided.
1970 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide

sequences have been determined. Because the cDNA of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

EP 1 308 459 A2

UTERU20140010
 UTERU20167570
 UTERU20168960//Homo sapiens actin filament associated protein (AFAP) mRNA, complete cds.//2.60E-68//364aa//43%//AF188700
 5 UTERU20169020//HOMEobox PROSPERO-LIKE PROTEIN PROX1 (PROX 1).//1.30E-54//117aa//74%//Q91018
 UTERU20173030
 UTERU20176230
 UTERU20177150//Homo Sapiens zinc finger protein dp mRNA, complete cds.//4.60E-10//104aa//40%//AF153201
 UTERU20181270
 10 UTERU20185220//Human mRNA for transcriptional activator hSNF2a, complete cds.//1.60E-125//246aa//98%//D26155
 UTERU20188670//HFM1 PROTEIN.//5.10E-19//234aa//26%//P51979
 UTERU20188840

15

Claims

1. A polynucleotide selected from the group consisting of the following (a) to (g):
 - 20 (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970;
 - (b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1971 to 3940;
 - (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1971 to 3940, wherein, in said amino acid sequence, one or more amino acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;
 - (d) a polynucleotide hybridizing to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;
 - (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);
 - (f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970; and
 - (g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970.
2. A polypeptide encoded by the polynucleotide of claim 1, or a partial peptide thereof.
- 40 3. An antibody binding to the polypeptide or the peptide of claim 2.
4. A method for immunologically assaying the polypeptide or the peptide of claim 2, said method comprising the steps of contacting the polypeptide or the peptide of claim 2 with the antibody of claim 3, and observing the binding between the two.
- 45 5. A vector comprising the polynucleotide of claim 1.
6. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5.
- 50 7. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5 in an expressible manner.
8. A method for producing the polypeptide or the peptide of claim 2, said method comprising the steps of culturing the transformant of claim 7 and recovering an expression product.
- 55 9. An oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1970 or to a complementary strand thereof.

10. Use of the oligonucleotide of claim 9 as a primer for synthesizing the polynucleotide of claim 1.
11. Use of the oligonucleotide of claim 9 as a probe for detecting the polynucleotide of claim 1.
- 5 12. An antisense polynucleotide against the polynucleotide of claim 1 or a part thereof.
13. A method for detecting the polynucleotide of claim 1, said method comprising the following steps of:
 - 10 a) incubating a target polynucleotide with the oligonucleotide of claim 9 under hybridizable conditions, and
 - b) detecting hybridization of the target polynucleotide with the oligonucleotide of claim 9.
14. A database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 1970 and/or on at least one of the amino acid sequences of SEQ ID NOs: 1971 to 3940.

15

20

25

30

35

40

45

50

55